Neutrokine-α

```
1   AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60

61  ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120

121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
1                           M  D  D  S  T  E  R  E  Q  S  R  L  12

181 TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC 240
13    T  S  C  L  K  K  R  E  E  M  K  L  K  E  C  V  S  I  L  P  32
                                                      CD-I

241 CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT 300
33    R  K  E  S  P  S  V  R  S  S  K  D  G  K  L  L  A  A  T  L  52
                    CD-I

301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC 360
53    L  L  A  L  L  S  C  C  L  T  V  V  S  F  Y  Q  V  A  A  L  72

361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420
73    Q  G  D  L  A  S  L  R  A  E  L  Q  G  H  H  A  E  K  L  P  92
                    CD-II

421 CAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC 480
93    A  G  A  G  A  P  K  A  G  L  E  E  A  P  A  V  T  A  G  L  112
                    CD-III
                                  #
481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
113   K  I  F  E  P  P  A  P  G  E  G  N  S  S  Q  N  S  R  N  K  132

541 AGCGTGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600
133   R  A  V  Q  G  P  E  E  T  V  T  Q  D  C  L  Q  L  I  A  D  152
                                                      CD-IV
```

FIG.1A

Neutrokine-α

```
601  ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT  660
153    S  E  T  P  T  I  Q  K  G  S  Y  T  F  V  P  W  L  L  S  F  172
                                              CD-V

661  TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT  720
173    K  R  G  S  A  L  E  E  K  E  N  K  I  L  V  K  E  T  G  Y  192
          CD-V                                 CD-VI

721  ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA  780
193    F  F  I  Y  G  Q  V  L  Y  T  D  K  T  Y  A  M  G  H  L  I  212
                      CD-VI                              CD-VII

781  TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT  840
213    Q  R  K  K  V  H  V  F  G  D  E  L  S  L  V  T  L  F  R  C  232
          CD-VII                                 CD-VIII

                              #
841  GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA  900
233    I  Q  N  M  P  E  T  L  P  N  N  S  C  Y  S  A  G  I  A  K  252
          CD-VIII                              CD-IX

901  AACTGGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAATGCACAAATATCAC  960
253    L  E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L  272
                      CD-X

961  TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT  1020
273    D  G  D  V  T  F  F  G  A  L  K  L  L                     285
                         CD-XI

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA  1080

1081 CCAAAAAAAAAAAAAAAAAA  1100
```

FIG.1B

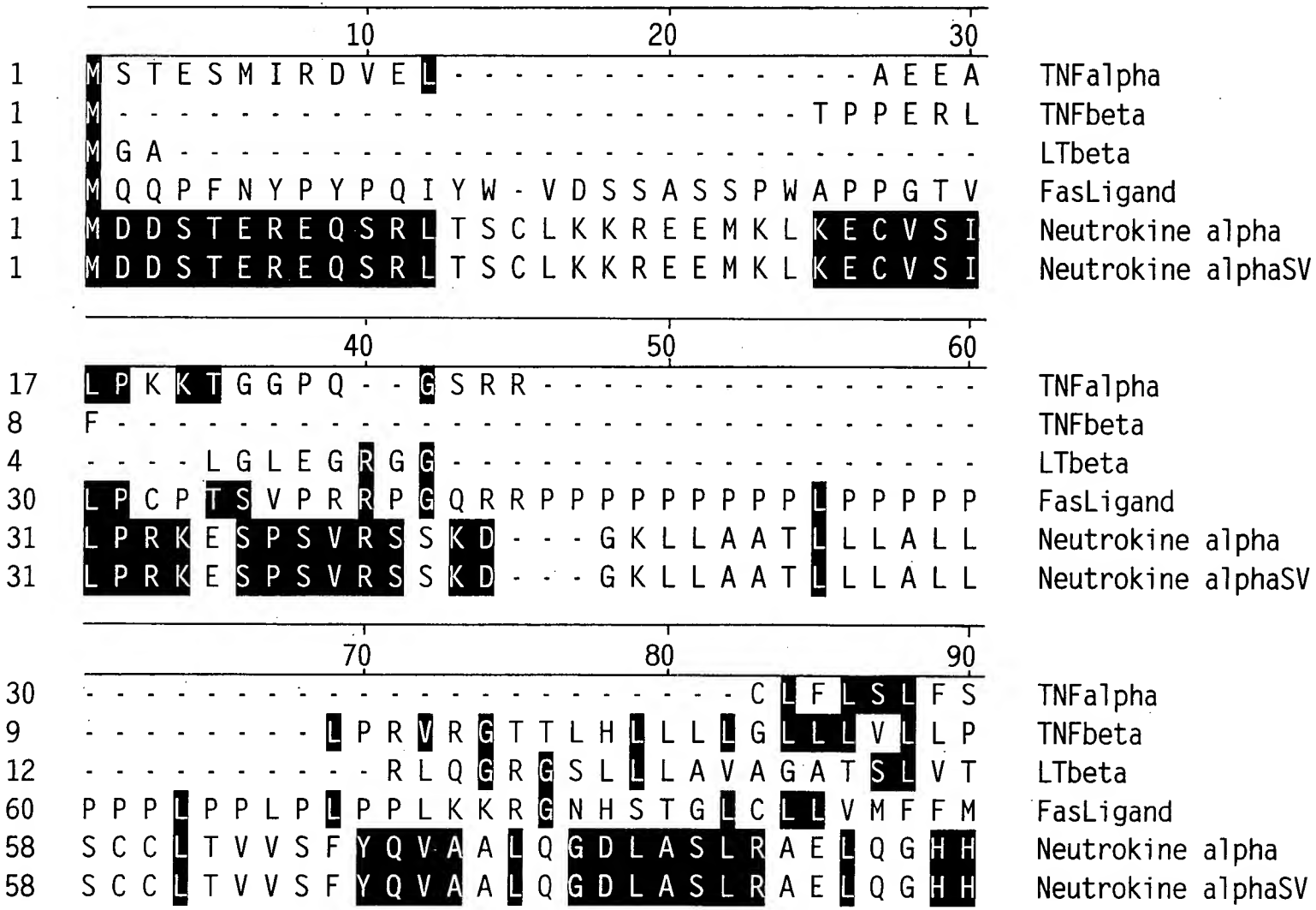
10 20 30
1 MSTESMIRDVEL----------AEEA TNFalpha
1 M----------TPPERL TNFbeta
1 MGA---------- LTbeta
1 MQQPFNYPYPQIYW-VDSSASSPWAPPGTV FasLigand
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alpha
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alphaSV
40 50 60
17 LPKKTGGPQ--GSRR---------- TNFalpha
8 F---------- TNFbeta
4 ----LGLEGRGG---------- LTbeta
30 LPCPTSVPRRPGQRRPPPPPPPPPPLPPPPP FasLigand
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alpha
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alphaSV
70 80 90
30 ----------CLFLSLFS TNFalpha
9 ---------LPRVRGTTLHLLLLGLLLVLLP TNFbeta
12 ----------RLQGRGSLLLAVAGATSLVT LTbeta
60 PPPLPPLPLPPLKKRGNHSTGLCLLVMFFM FasLigand
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alpha
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alphaSV

FIG.2A

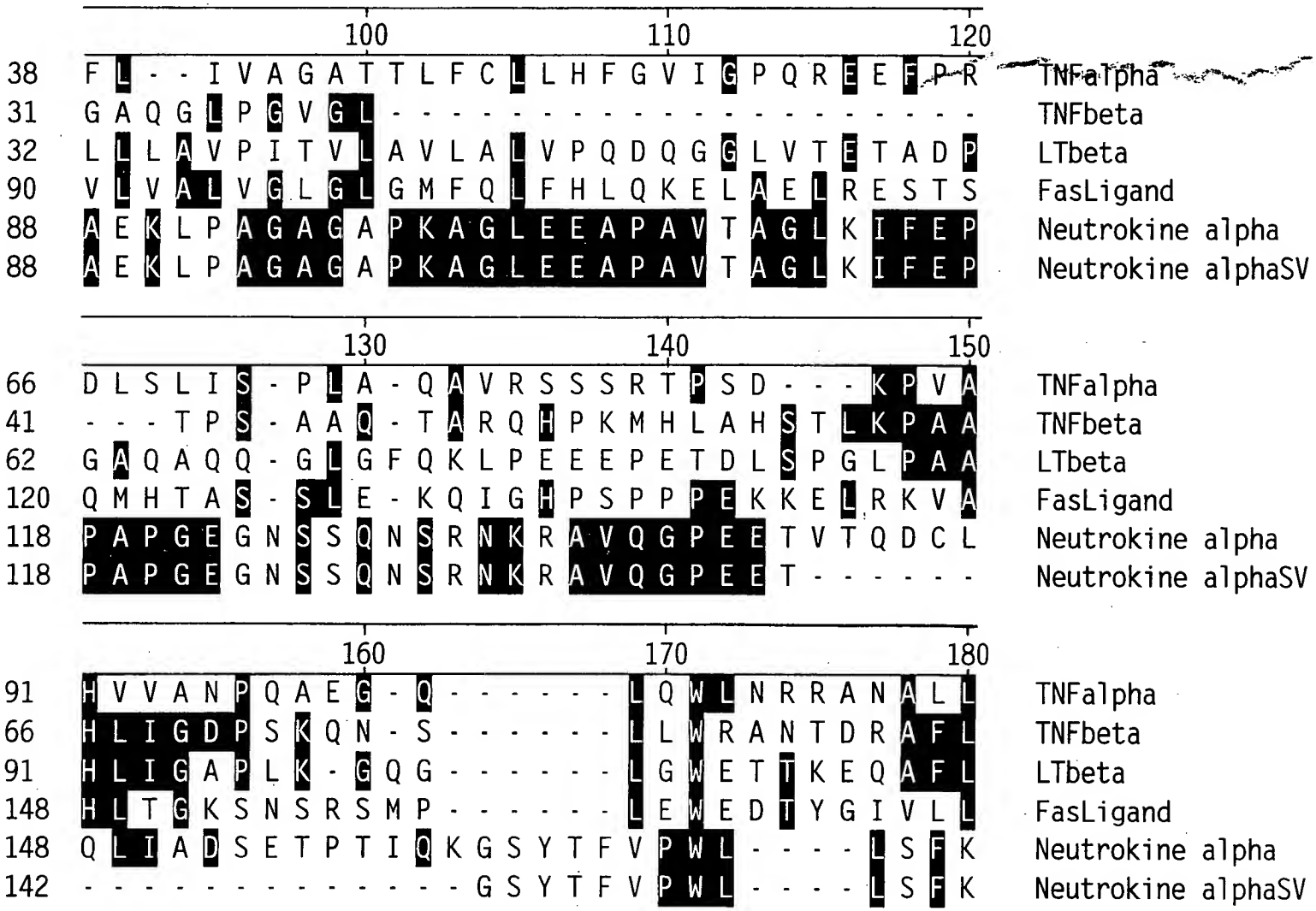
100 110 120
38 FL--IVAGATTLFCLLHFGVIGPQREEFPR TNFalpha
31 GAQGLPGVGL---------- TNFbeta
32 LLLAVPITVLAVLALVPQDQGGLVTETADP LTbeta
90 VLVALVGLGLGMFQLFHLQKELAELRESTS FasLigand
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alpha
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alphaSV
130 140 150
66 DLSLIS-PLA-QAVRSSSRTPSD---KPVA TNFalpha
41 ---TPS-AAQ-TARQHPKMHLAHSTLKPAA TNFbeta
62 GAQAQQ-GLGFQKLPEEEPETDLSPGLPAA LTbeta
120 QMHTAS-SLE-KQIGHPSPPPEKKELRKVA FasLigand
118 PAPGEGNSSQNSRNKRAVQGPEETVTQDCL Neutrokine alpha
118 PAPGEGNSSQNSRNKRAVQGPEET------ Neutrokine alphaSV
160 170 180
91 HVVANPQAEG-Q------LQWLNRRANALL TNFalpha
66 HLIGDPSKQN-S------LLWRANTDRAFL TNFbeta
91 HLIGAPLK-GQG------LGWETTKEQAFL LTbeta
148 HLTGKSNSRSMP------LEWEDTYGIVLL FasLigand
148 QLIADSETPTIQKGSYTFVPWL----LSFK Neutrokine alpha
142 ----------GSYTFVPWL----LSFK Neutrokine alphaSV

FIG.2B

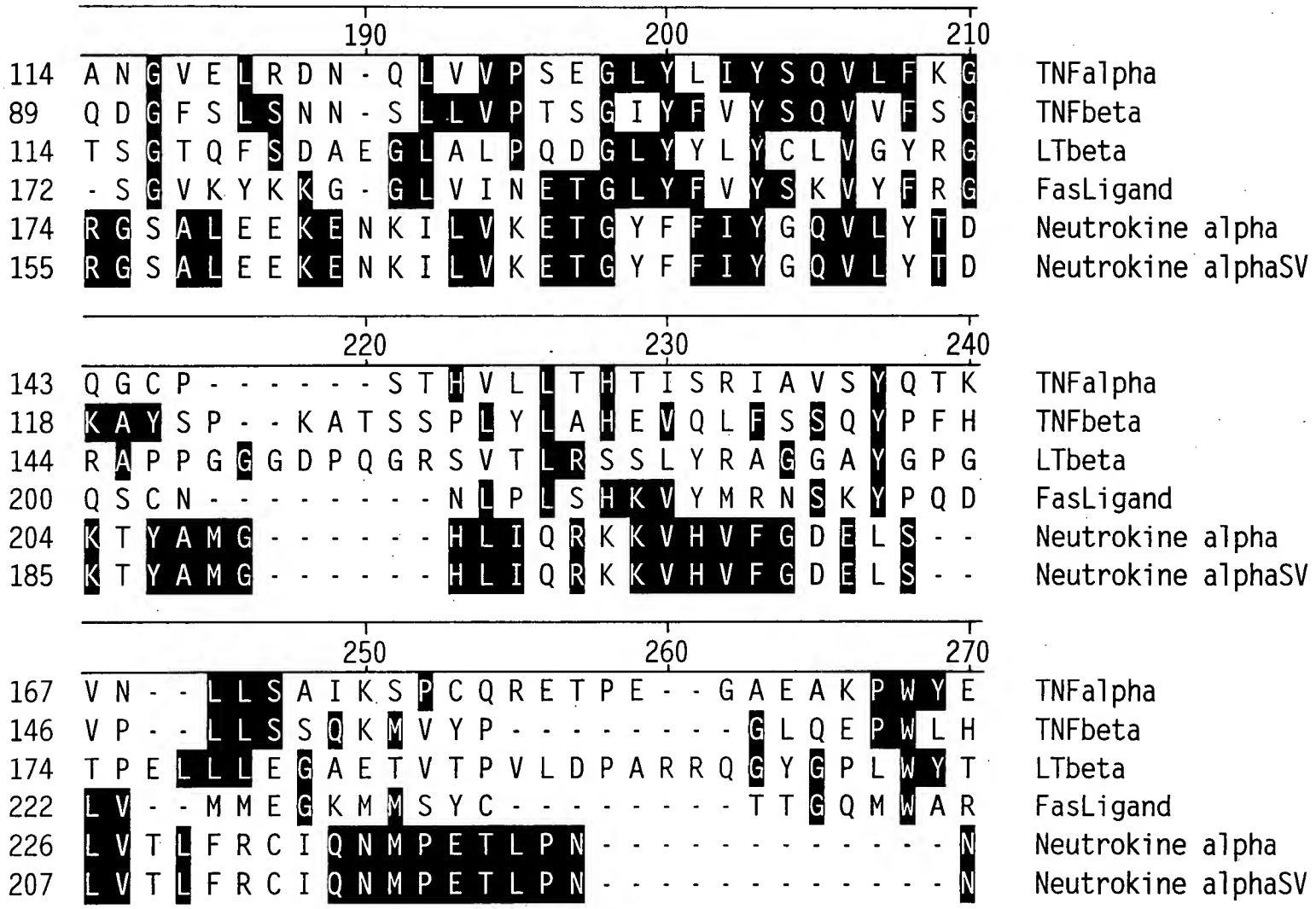
190 200 210
114 ANGVELRDN-QLVVPSEGLYLIYSQVLFKG TNFalpha
89 QDGFSLSNN-SLLVPTSGIYFVYSQVVFSG TNFbeta
114 TSGTQFSDAEGLALPQDGLYYLYCLVGYRG LTbeta
172 -SGVKYKKG-GLVINETGLYFVYSKVYFRG FasLigand
174 RGSALEEKENKILVKETGYFFIYGQVLYTD Neutrokine alpha
155 RGSALEEKENKILVKETGYFFIYGQVLYTD Neutrokine alphaSV
220 230 240
143 QGCP------STHVLLTHTISRIAVSYQTK TNFalpha
118 KAYSP--KATSSPLYLAHEVQLFSSQYPFH TNFbeta
144 RAPPGGGDPQGRSVTLRSSLYRAGGAYGPG LTbeta
200 QSCN---------NLPLSHKVYMRNSKYPQD FasLigand
204 KTYAMG------HLIQRKKVHVFGDELS-- Neutrokine alpha
185 KTYAMG------HLIQRKKVHVFGDELS-- Neutrokine alphaSV
250 260 270
167 VN--LLSAIKSPCQRETPE--GAEAKPWYE TNFalpha
146 VP--LLSSQKMVYP---------GLQEPWLH TNFbeta
174 TPELLLEGAETVTPVLDPARRQGYGPLWYT LTbeta
222 LV--MMEGKMMSYC---------TTGQMWAR FasLigand
226 LVTLFRCIQNMPETLPN----------------N Neutrokine alpha
207 LVTLFRCIQNMPETLPN----------------N Neutrokine alphaSV

FIG.2C

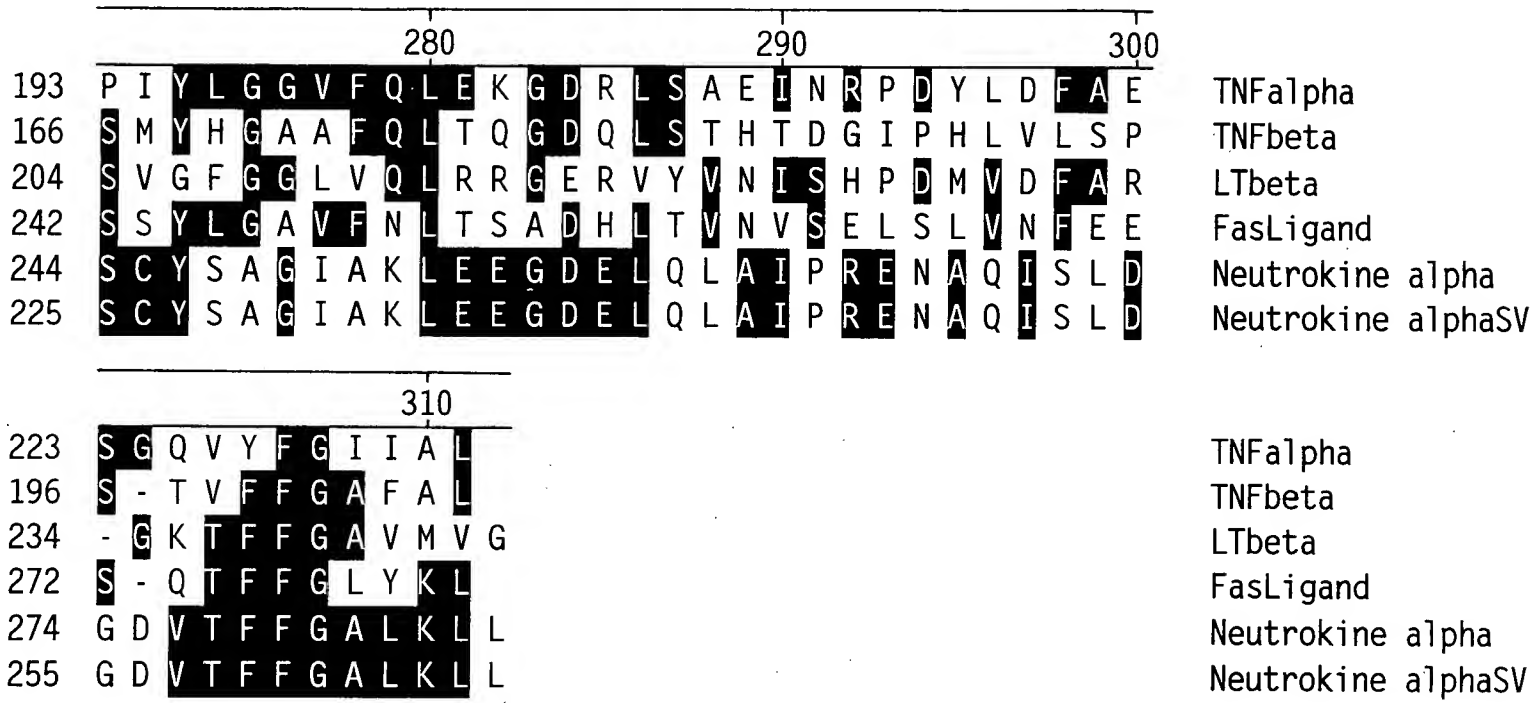
280
290
300
193 P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E TNFalpha
166 S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P TNFbeta
204 S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R LTbeta
242 S S Y L G A V F N L T S A D H L T V N V S E L S L V N F E E FasLigand
244 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D Neutrokine alpha
225 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D Neutrokine alphaSV
310
223 S G Q V Y F G I I A L TNFalpha
196 S - T V F F G A F A L TNFbeta
234 - G K T F F G A V M V G LTbeta
272 S - Q T F F G L Y K L FasLigand
274 G D V T F F G A L K L L Neutrokine alpha
255 G D V T F F G A L K L L Neutrokine alphaSV

FIG.2D

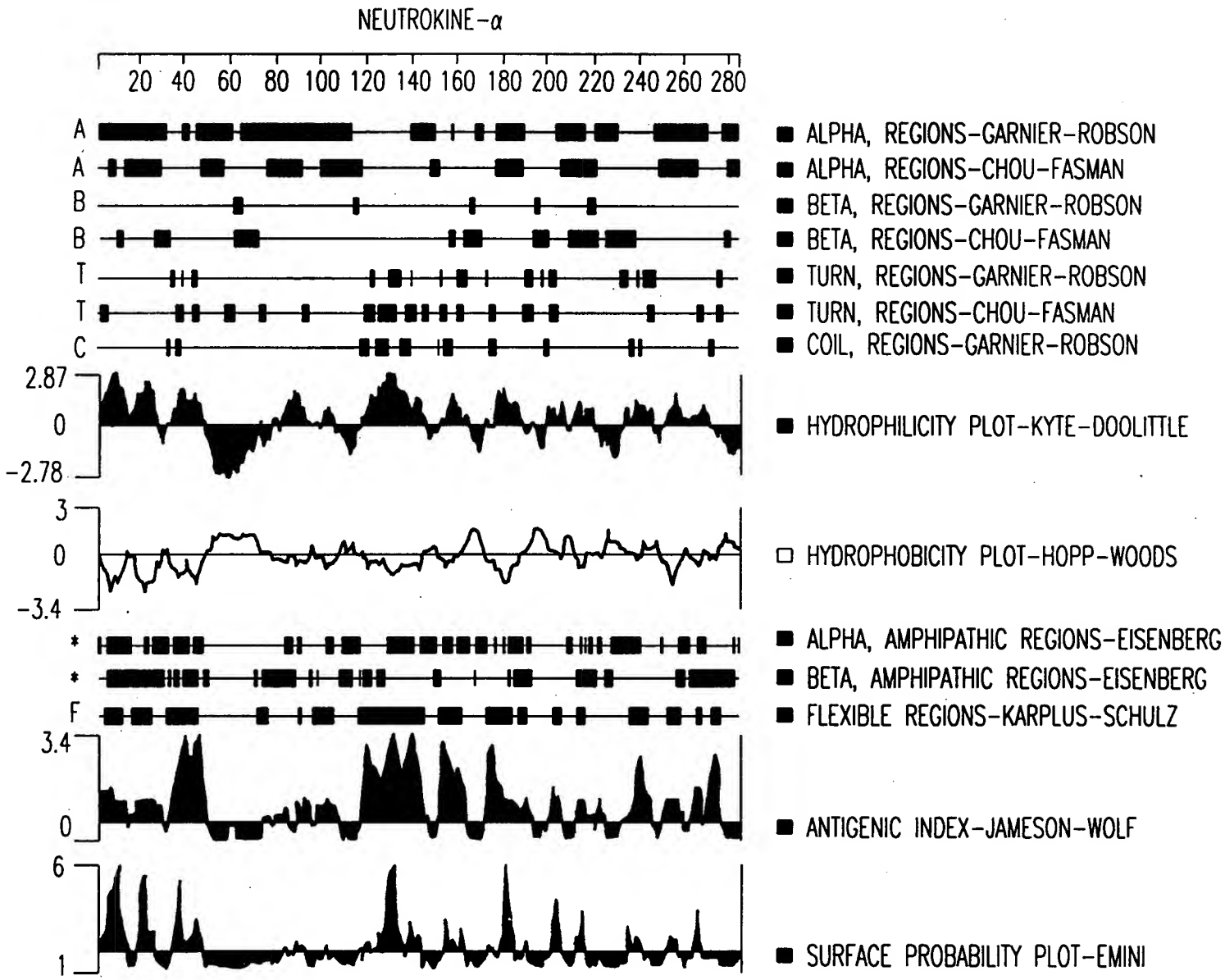
NEUTROKINE-α
20 40 60 80 100 120 140 160 180 200 220 240 260 280
A
A
B
B
T
T
C
2.87
0
-2.78
3
0
-3.4
*
*
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.3

```
          1                                                   50
HSOAD55R  .........A GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HNEDU15X  ...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HSLAH84R  .AATTCGGCA NAGNAAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT
HLTBM08R  AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG

          51                                                  100
HSOAD55R  GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC
HNEDU15X  GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC
HSLAH84R  ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC
HLTBM08R  GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA

          101                                                 150
HSOAD55R  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HNEDU15X  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HSLAH84R  CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA
HLTBM08R  GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC

          151                                                 200
HSOAD55R  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HNEDU15X  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HSLAH84R  AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG
HLTBM08R  AAGACTGCTT GCAACTGNTT GCAGACAGTG AAACACCAAC TATACAAAAA

          201                                                 250
HSOAD55R  AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG
HNEDU15X  AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG
HSLAH84R  CAAAACTGGN AGGAAGGA.. ...GATGAAC TCCAACTTGC AATACCAGGG
HLTBM08R  GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG

          251                                                 300
HSOAD55R  GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HNEDU15X  GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HSLAH84R  GAAAATGCAC AATTATCACT GGGATGGAGA TGTTCACATT TTTTGGGTGC
HLTBM08R  TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTTNCT CTCTGGGAAT

          301                                                 350
HSOAD55R  CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTTNTT.
HNEDU15X  CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC
HSLAH84R  CATTGAAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC
HLTBM08R  CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT

          351                                                 400
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT
HSLAH84R  CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA
HLTBM08R  AAGTTTTAAA AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC
```

FIG.4A

```
          401                                                       450
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  GCAGGGCCAC CACGCGGAGA AGCTGCCAGC AGGAGCAGGA GCCCCCAAGG
HSLAH84R  ATAACCCAAA AAAANNTTAA ANGGGTANGN GNNANANGNG GGGNNGTTNN
HLTBM08R  CAAGGNACTG GTTANTTTNT AAATATGGTC AGGTTTNTAT ANCTGGTAGG

          451                                                       500
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  CCGGCCTGGA GGAAGCTCCA GCTGTCACCG CGGGACTGAA AATCTTTGAA
HSLAH84R  CNNGNNGNNT TTTNGGNNTA TNTTNTNNTN GGGNNNNGTA AAAATGGGGC
HLTBM08R  CCTCGCCATG GGCATTNATT CANGGNGAGG NCNNTCTTTT GGGNTGA...

          501                                                       550
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  CCACCAGCTC CAGGAGAAGG CAACTCCAGT CAGAACAGCA GAAATAAGCG
HSLAH84R  CNANGGGGGN TTTTT..... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

          551                                                       600
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TGCCGTTCAG GGTCCAGAAG AAACAGTCAC TCAAGACTGC TTGCAACTGA
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

          601                                                       650
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TTGCAGACAG TGAAACACCA ACTATACAAA AAGGATCTTA CACATTTGTT
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

          651                                                       700
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  CCATGGCTTC TCAGCTTTAA AAGGGGAAGT GCCCTAGAAG AAAAAGAGAA
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

          701                                                       750
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TAAAATATTG GTCAAAGAAA CTGGTTACTT TTTTATATAT GGTCAGGTTT
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

          751                                                       800
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TATATACTGA TAAGACCTAC GCCATGGGAC ATCTAATTCA GAGGAAGAAG
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........
```

FIG.4B

```
            801                                                       850
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GTCCATGTCT TTGGGGATGA ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            851                                                       900
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TCAAAATATG CCTGAAACAC TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            901                                                       950
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAAAACT GGAAGAAGGA GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            951                                                      1000
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    AATGCACAAA TATCACTGGA TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1001                                                     1050
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    ACTGCTGTGA CCTACTTACA CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1051                                                     1100
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CTGTACCTCT AAGAAGAAAG AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1101
HSOAD55R    ......
HNEDU15X    AAAAAA
HSLAH84R    ......
HLTBM08R    ......
```

FIG.4C

Neutrokine-αSV

```
  1  ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA  60
  1  M  D  D  S  T  E  R  E  Q  S  R  L  T  S  C  L  K  K  R  E   20

 61  GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGA 120
 21  E  M  K  L  K  E  C  V  S  I  L  P  R  K  E  S  P  S  V  R   40
                                    CD-I

121  TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC 180
 41  S  S  K  D  G  K  L  L  A  A  T  L  L  L  A  L  L  S  C  C   60
       CD-I

181  CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG 240
 61  L  T  V  V  S  F  Y  Q  V  A  A  L  Q  G  D  L  A  S  L  R   80
                                          CD-II

241  GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC 300
 81  A  E  L  Q  G  H  H  A  E  K  L  P  A  G  A  G  A  P  K  A  100
     CD-II                                    CD-III

301  GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA 360
101  G  L  E  E  A  P  A  V  T  A  G  L  K  I  F  E  P  P  A  P   120
   CD-III
            #
361  GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAA 420
121  G  E  G  N  S  S  Q  N  S  R  N  K  R  A  V  Q  G  P  E  E   140

421  ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA 480
141  T  G  S  Y  T  F  V  P  W  L  L  S  F  K  R  G  S  A  L  E   160
                                       CD-IV

481  GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATATGGTCAGGTT 540
161  E  K  E  N  K  I  L  V  K  E  T  G  Y  F  F  I  Y  G  Q  V   180
     CD-IV                          CD-V

541  TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC 600
181  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q  R  K  K  V  H  V   200
                CD-VI                    CD-VII
```

FIG.5A

Neutrokine-αSV

```
601  TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA  660
201  F  G  D  E  L  S  L  V  T  L  F  R  C  I  Q  N  M  P  E  T   220
     CD-VIII                    CD-VIII

661  CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC  720
221  L  P  N  N  S  C  Y  S  A  G  I  A  K  L  E  E  G  D  E  L   240
                  CD-IX                       CD-X

721  CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT  780
241  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D  G  D  V  T  F  F   260
        CD-X                                                CD-XI

781  GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC  840
261  G  A  L  K  L  L                                            266
        CD-XI

841  TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAA  900

901  AAA  903
```

FIG.5B

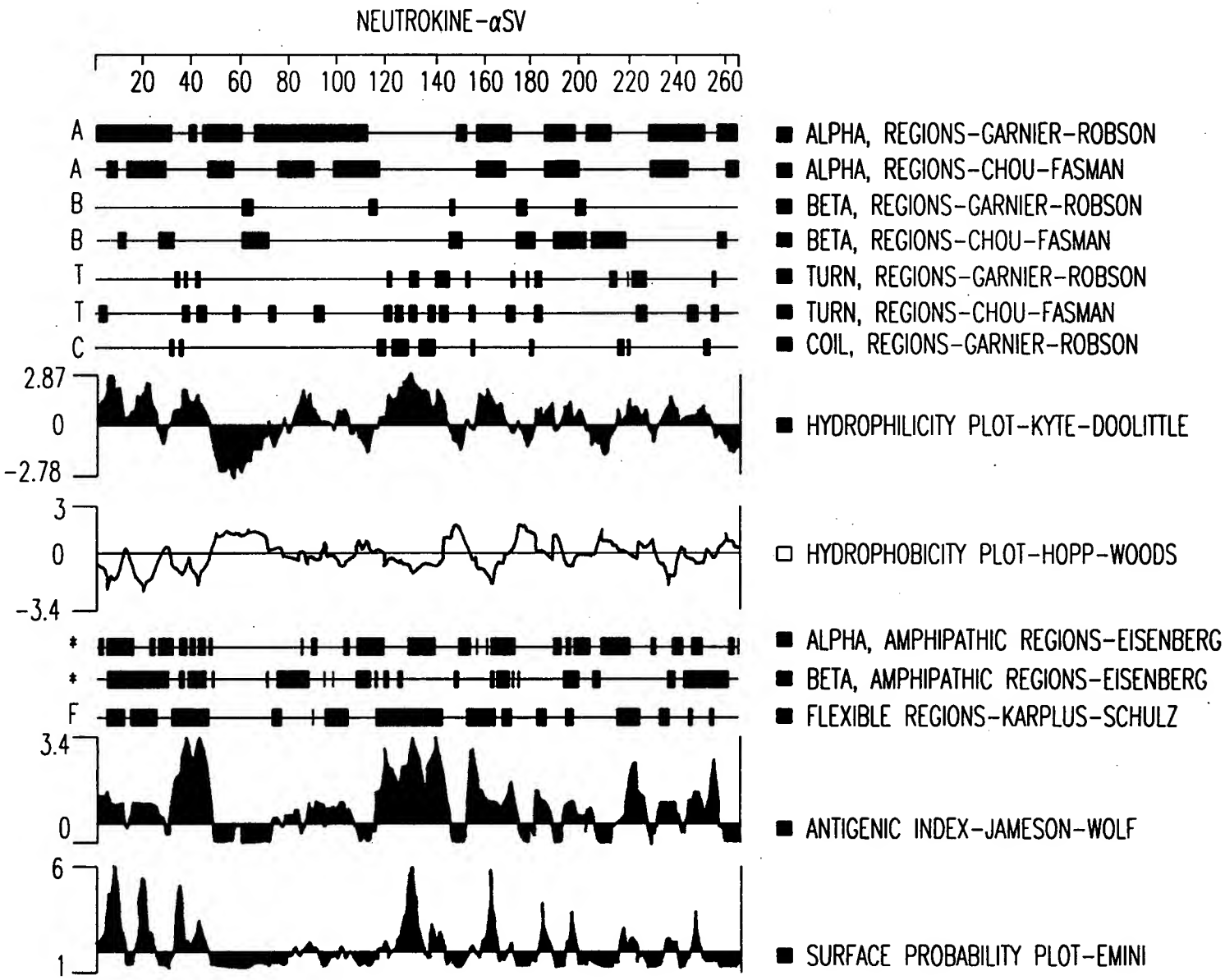
NEUTROKINE-αSV
20 40 60 80 100 120 140 160 180 200 220 240 260
A
A
B
B
T
T
C
2.87
0
-2.78
3
0
-3.4
*
*
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.6

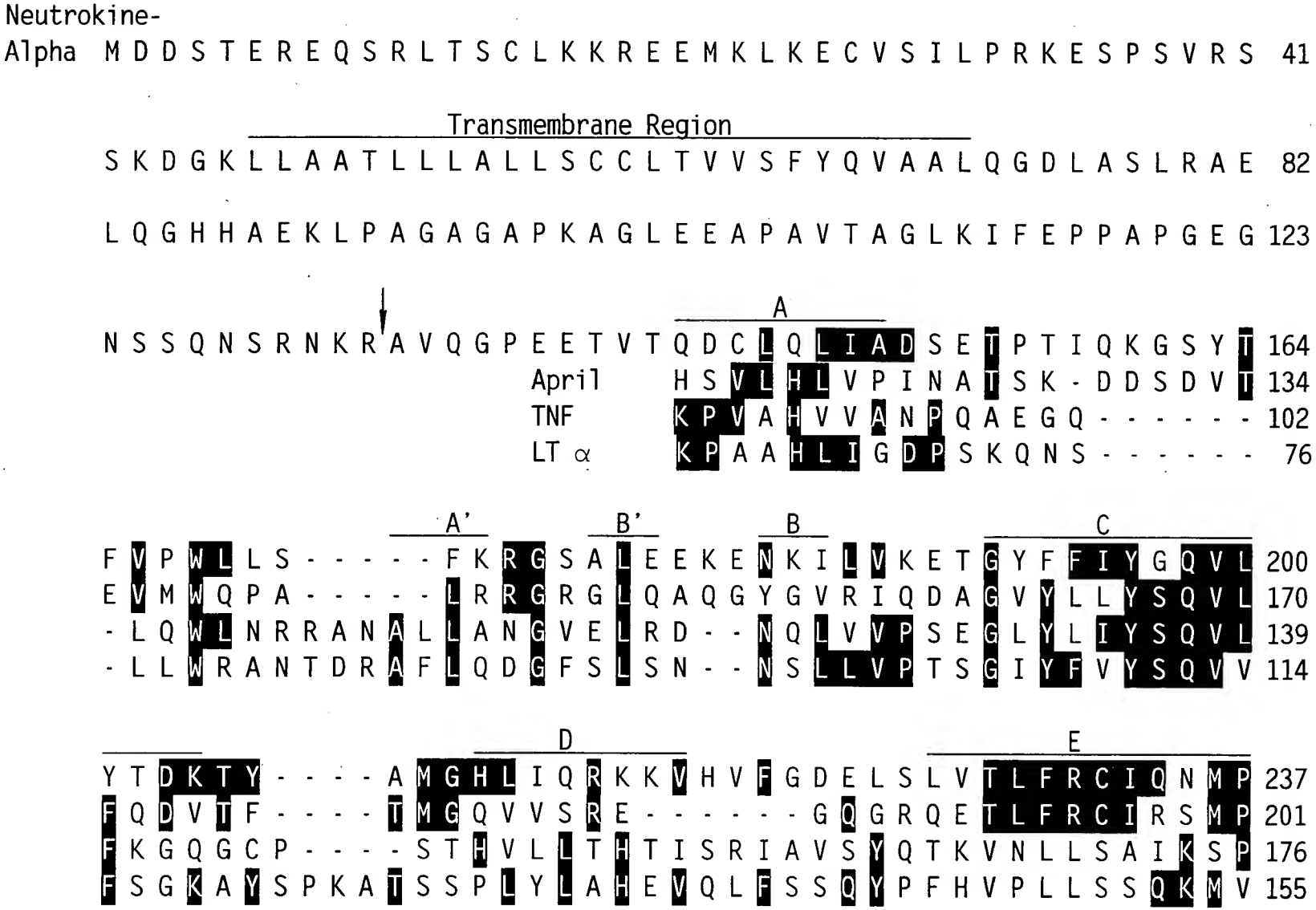
Neutrokine-
Alpha M D D S T E R E Q S R L T S C L K K R E E M K L K E C V S I L P R K E S P S V R S 41
Transmembrane Region
S K D G K L L A A T L L L A L L S C C L T V V S F Y Q V A A L Q G D L A S L R A E 82
L Q G H H A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P P A P G E G 123
A
N S S Q N S R N K R A V Q G P E E T V T Q D C L Q L I A D S E T P T I Q K G S Y T 164
April H S V L H L V P I N A T S K - D D S D V T 134
TNF K P V A H V V A N P Q A E G Q - - - - - - 102
LT α K P A A H L I G D P S K Q N S - - - - - - 76
A' B' B C
F V P W L L S - - - - - F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L 200
E V M W Q P A - - - - - L R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L 170
- L Q W L N R R A N A L L A N G V E L R D - - N Q L V V P S E G L Y L I Y S Q V L 139
- L L W R A N T D R A F L Q D G F S L S N - - N S L L V P T S G I Y F V Y S Q V V 114
D E
Y T D K T Y - - - - A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q N M P 237
F Q D V T F - - - - T M G Q V V S R E - - - - - - G Q G R Q E T L F R C I R S M P 201
F K G Q G C P - - - - S T H V L L T H T I S R I A V S Y Q T K V N L L S A I K S P 176
F S G K A Y S P K A T S S P L Y L A H E V Q L F S S Q Y P F H V P L L S S Q K M V 155

FIG.7A-1

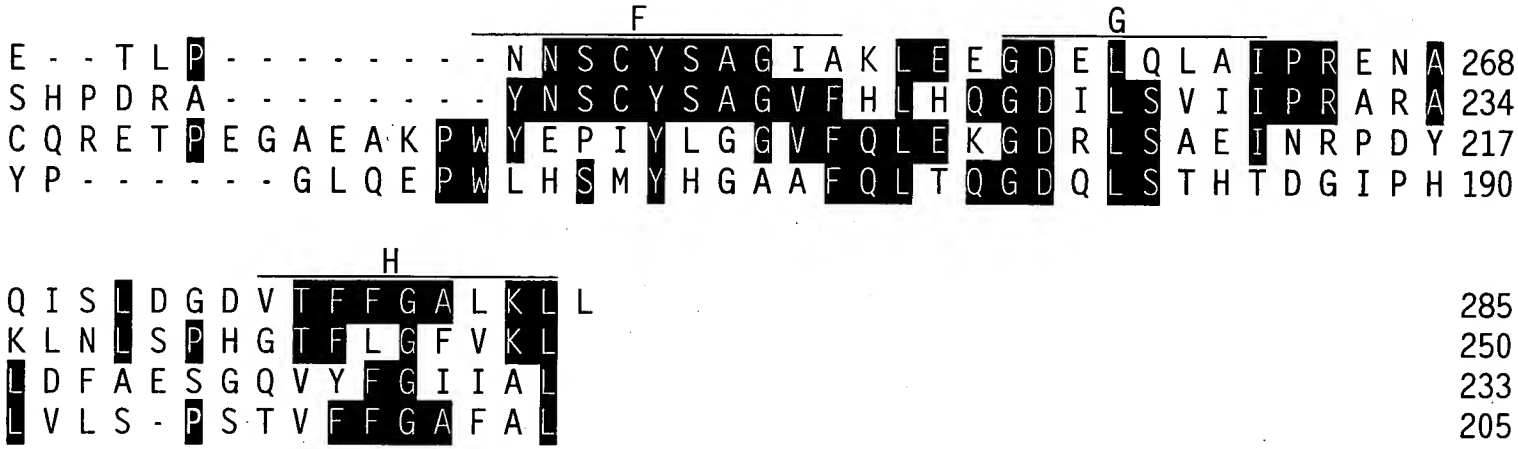
F
G
E--TLP---------NNSCYSAGIAKLEEGDELQLAIPRENA 268
SHPDRA---------YNSCYSAGVFHLHQGDILSVIIPRARA 234
CQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDY 217
YP------GLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPH 190
H
QISLDGDVTFFGALKLL 285
KLNLSPHGTFLGFVKL 250
LDFAESGQVYFGIIAL 233
LVLS-PSTVFFGAFAL 205

FIG.7A-2

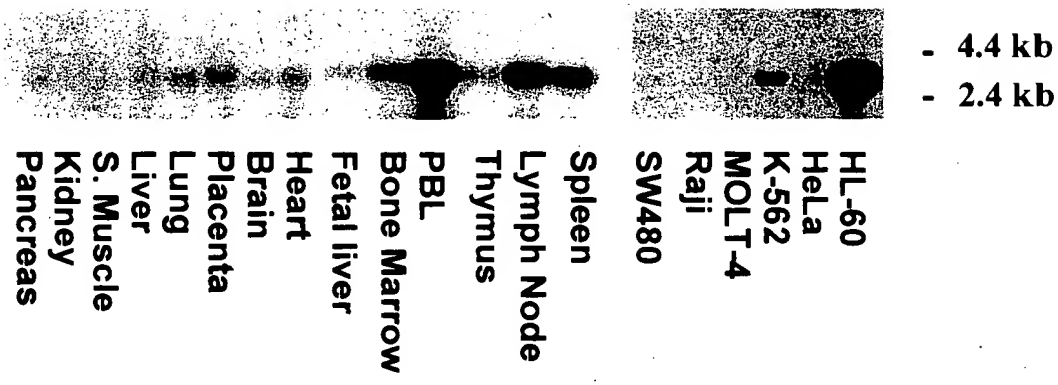
- 4.4 kb
- 2.4 kb
HL-60
HeLa
K-562
MOLT-4
Raji
SW480
Spleen
Lymph Node
Thymus
PBL
Bone Marrow
Fetal liver
Heart
Brain
Placenta
Lung
Liver
S. Muscle
Kidney
Pancreas

FIG.7B

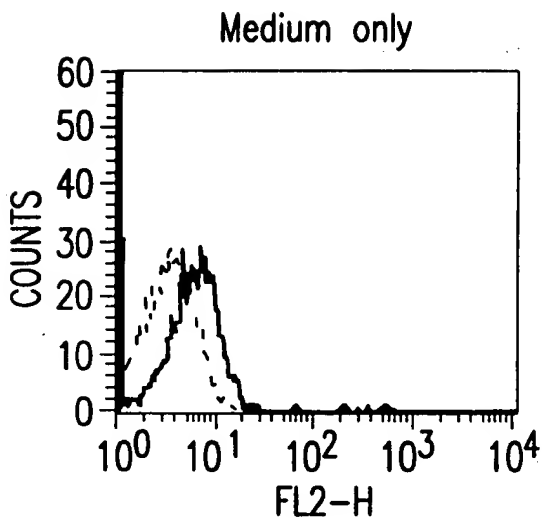

FIG.8A

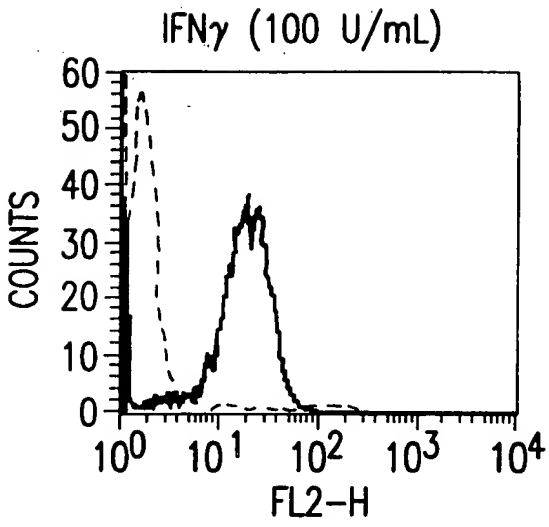

FIG.8B

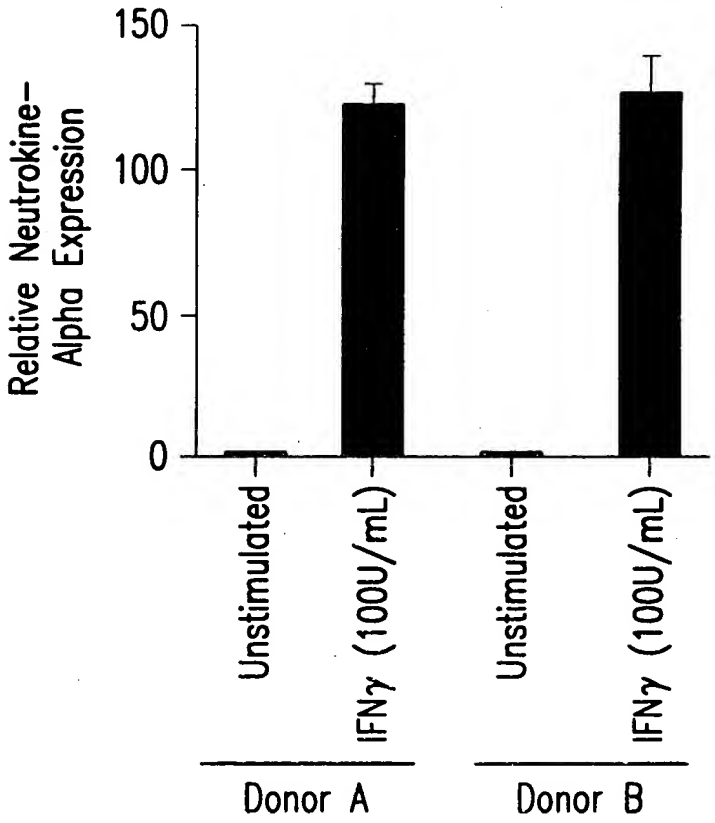

FIG.8C

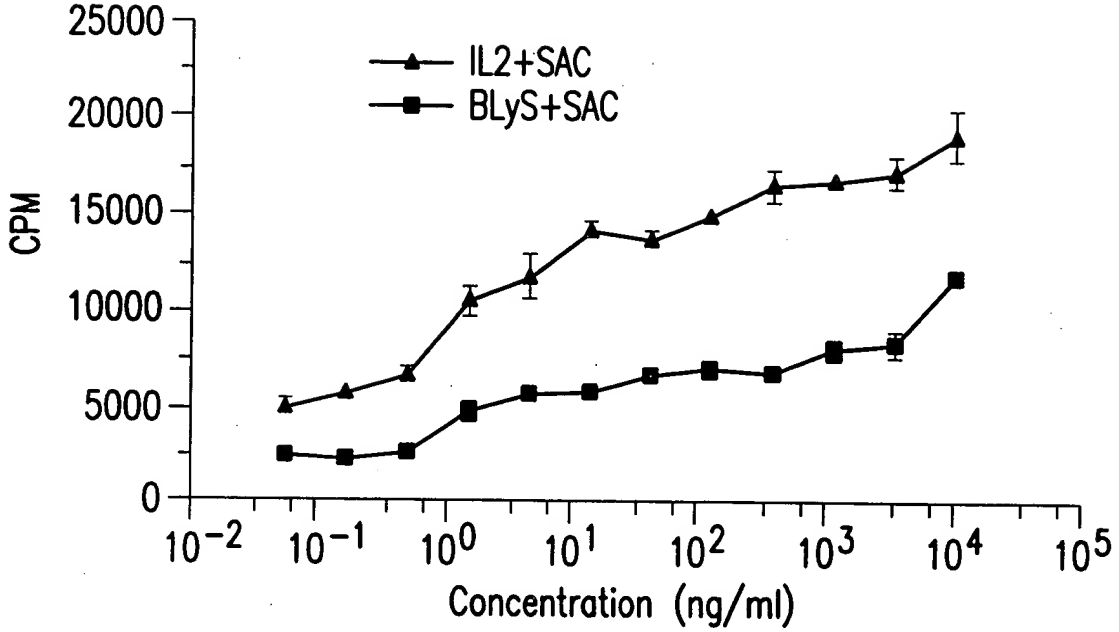
25000
20000
15000
10000
5000
0
CPM
IL2+SAC
BLyS+SAC
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
10^{5}
Concentration (ng/ml)

FIG. 9A

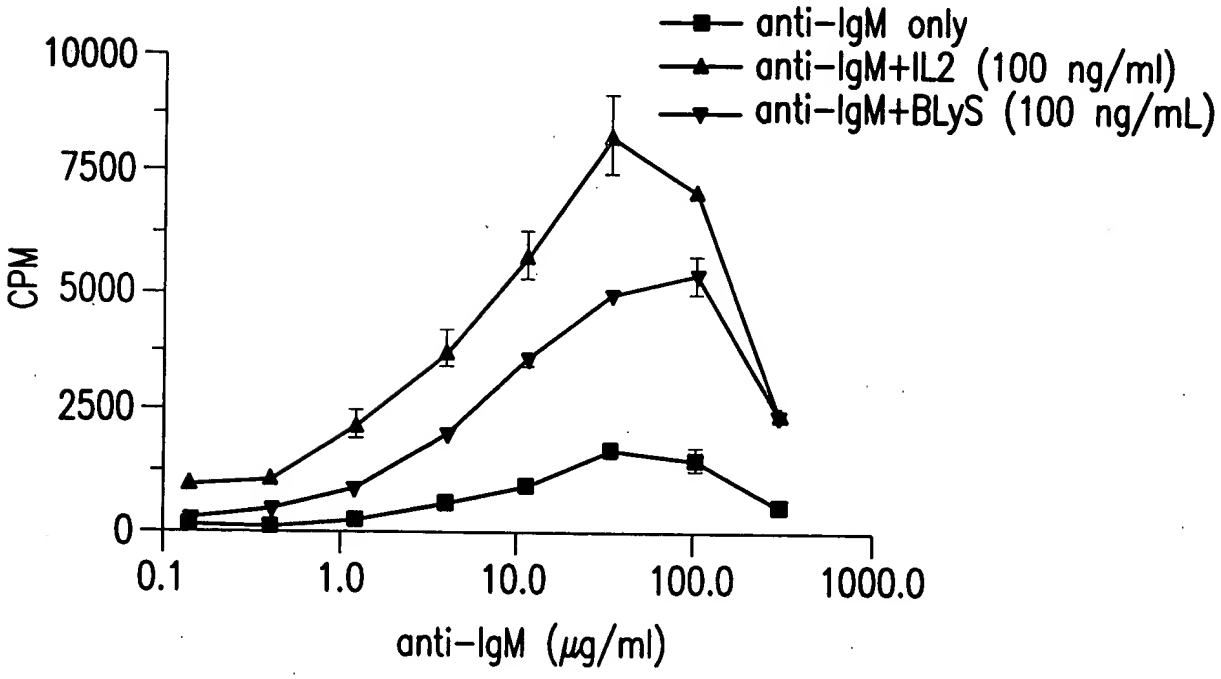
10000
7500
5000
2500
0
CPM
anti-IgM only
anti-IgM+IL2 (100 ng/ml)
anti-IgM+BLyS (100 ng/mL)
0.1
1.0
10.0
100.0
1000.0
anti-IgM (μg/ml)

FIG. 9B

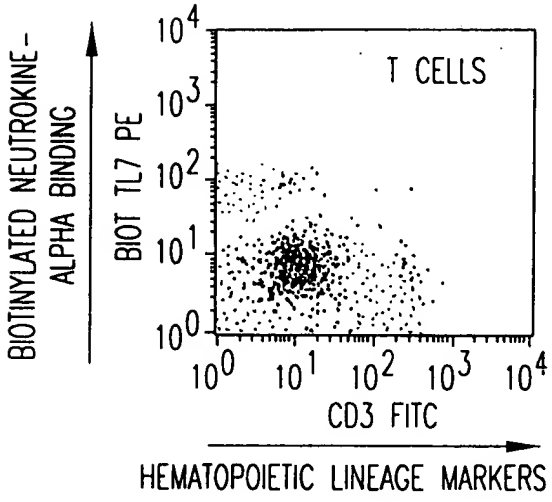

FIG.10A

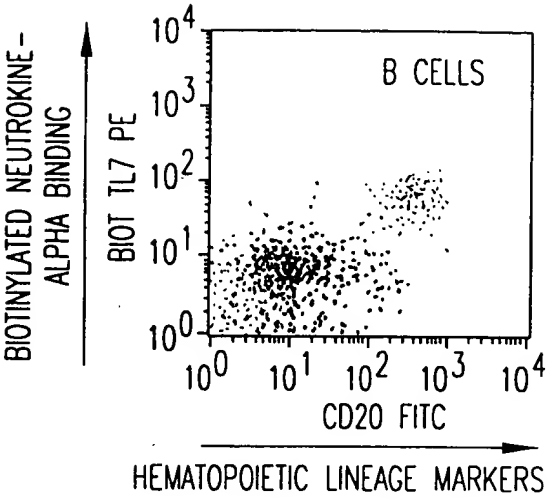

FIG.10B

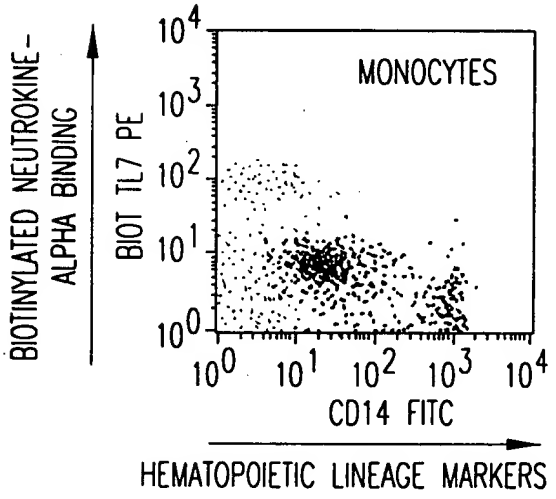

FIG.10C

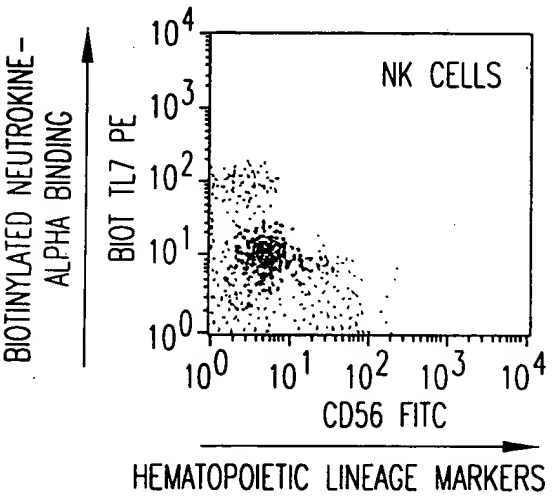

FIG.10D

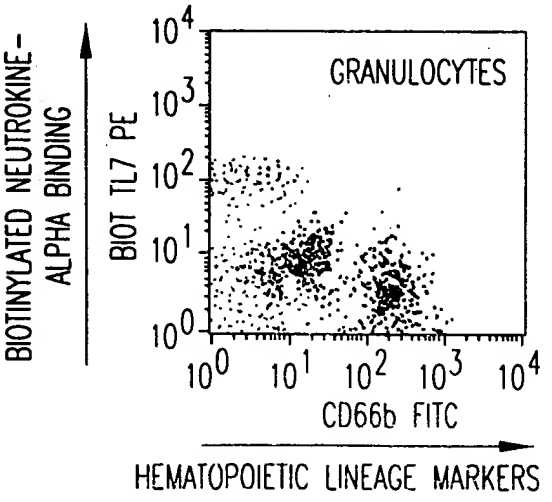

FIG.10E

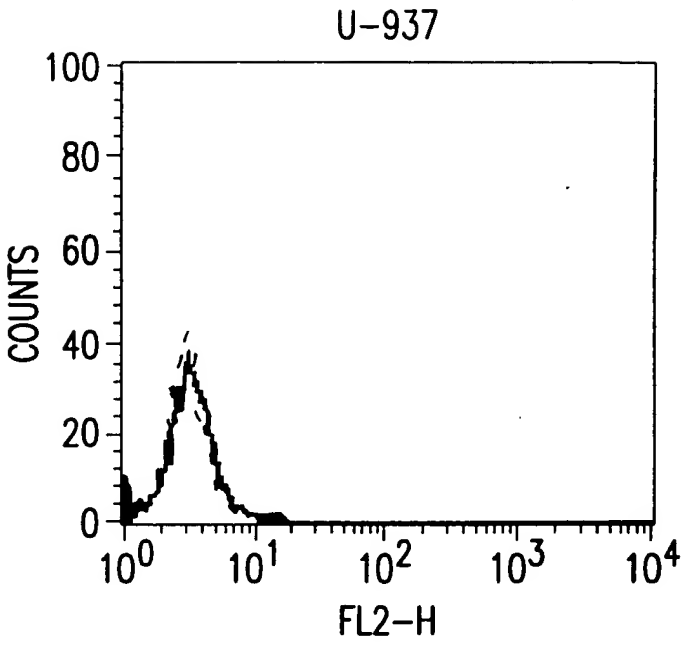

FIG.10F

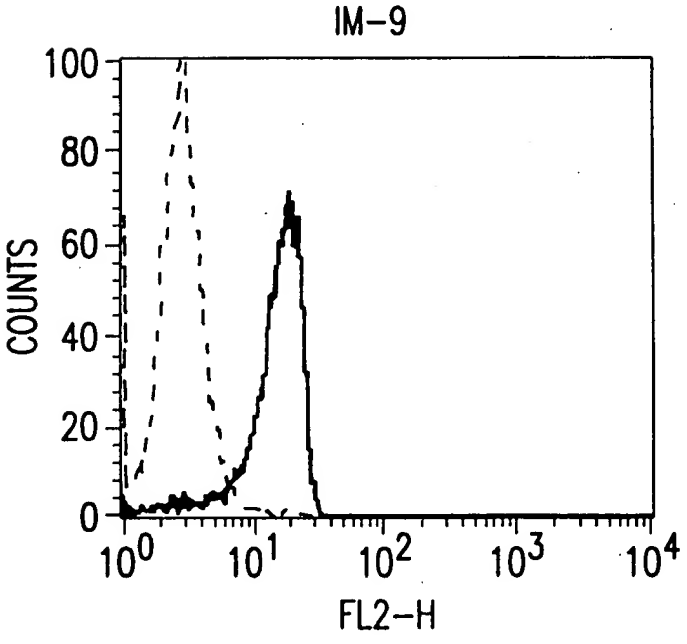

FIG.10G

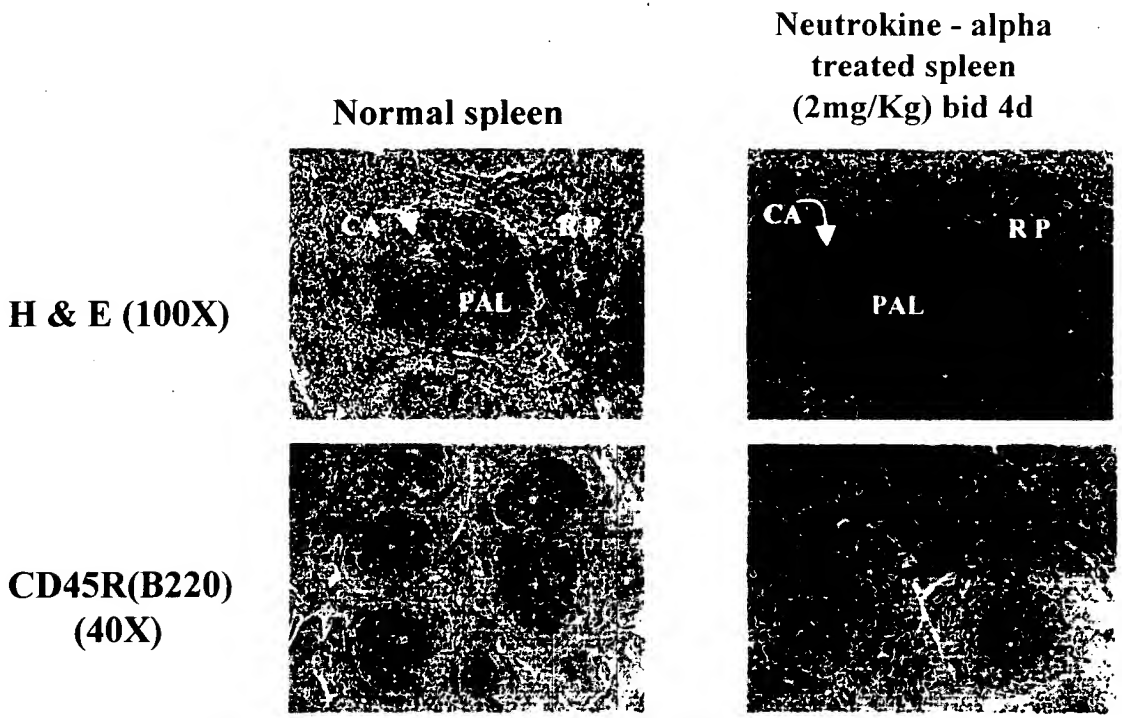
Normal spleen
Neutrokine - alpha treated spleen (2mg/Kg) bid 4d
H & E (100X)
CD45R(B220) (40X)
CA
RP
PAL
CA
RP
PAL

FIG.11A

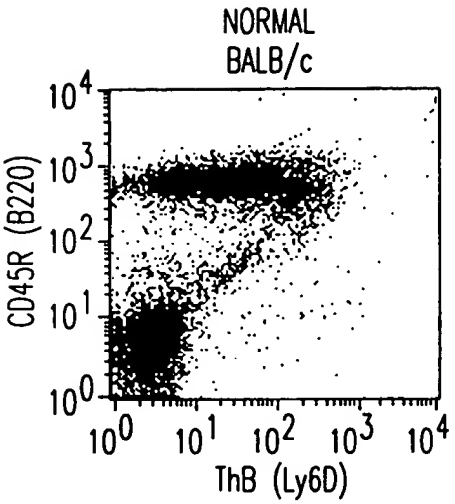

FIG. 11B

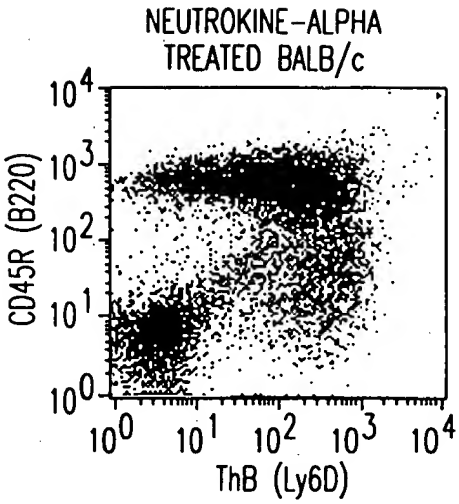

FIG. 11C

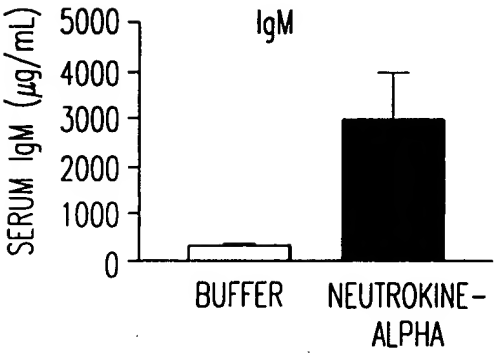

FIG. 11D

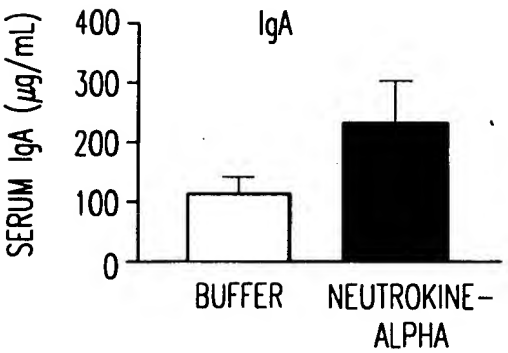

FIG. 11E

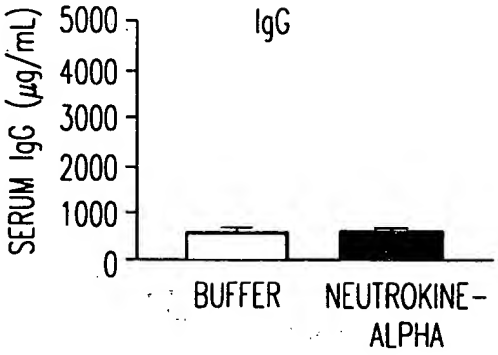

FIG. 11F